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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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94.8 4265

94.8 4265

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4.7 172027

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Description

DB

SUMMARIES

Homo sapi Homo sapi Rattus no Homo sapi

AL365274 PAF055883 PAL161906 P

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AB011283 Caenorhab
AB011279 Caenorhab
G21290 human STS W
AB011284 Caenorhab
AF051726 Mus muscu
                                                  AC011703 Drosophil
AC011492 Homo sapi
Z46266 Caenorhabdi
X89399 Homo sapien
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AC073765 Mus muscu
AB011285 Caenorhab
E13125 Bovine gene
U30857 Bos taurus
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S76368 ORF 5' of E
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           AC027051 Homo sapi
AC040900 Homo sapi
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Kim,J.H. and Huganir,R.L.
Kim,J.H. and Huganir,R.L.
Submitsed (09-APR-1998) Neuroscience, Johns Hopkins Medical
Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
Xim,J.H. and Huganir,R.L.
                               AC027051 Homo sapi
U20238 Mus musculu
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Submitted (08-0CT-1998) Neuroscience, Johns Hopkins Medical
Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
Sequence update by submitter
On Oct 9, 1998 this sequence version replaced gi:3065890.
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 4140)
Kim,7-1.4. Liao,D., Lau,L.F. and Huganir,R.L.
SyndaR: a synaptic RasGAP that associates with the PSD-95/SAP90
protein family
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Rattus norvegicus SynGAP-b mRNA, complete cds.
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74; DB Score 4118.8; Pred. No. 0; Query Match BASE COUNT ORIGIN

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360 cgcttccgaagtgctgaccatgaccgggcccggctgatgcagagcttcaaggagtctcac 301 307 δ qq

420 toccatgagiccetgetgagicceageagigetgetgaggeeetggageteaacetggat 361 367 õ g

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Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete
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KEVFASWRLIKCAERGREDIADRILSASLEFRFICPAIMSPSLFGLMOEYPDEQTSFFL
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IIGRLMLVEEELRRDHPAMAEPLPEPKKRLLDAQVERQLPPLGPTNPRVTLAPPWNGL
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Kim,J.H. and Huganir,R.L.
Birect Submission
Submitted (20-FEB-1998) Neuroscience, Johns Hopkins Medical
Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
On Sep 15, 2000 this sequence version replaced gi:3044054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Kim,J.H., Liboo,D., Lau,L.F. and Huganir,R.L.
SynGaP: a synaptic RasGAP that associates with the PSD-95/SAP90
protein family
Neuron 20 (4), 683-691 (1998)
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                                                                                                          4021 traaccccactgctccattccaggaggagagtgggaccctcagctgccctctcaccca
                                                                                                                                                                                                              /product="GTPase activating protein SynGAP-c"
/protein_id="AAC40082.2"
/db_xref="GI:10140855"
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/db_xref="taxon:10116"
/tissue_type="hippocampus"
/dev_stage="adult"
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                                            DB 74; Length 4265;
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                                           Score 3919; DB Pred. No. 0; 0; Mismatches
APPAPPPPRLQITENGEFRNTADH"
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28	GGGGGTAAAGACCTGTTCTATGTGAGCCGGCCACCACTGGCCGGTCCTCCCCCAGCATAC 2217
78 tgc    18 TGC	cacgagcagctcggacatcacagagccggggcagaagatgctgagtgtcaacaagagt 2337 
338 gt    278 GT	tgtccatgctggacctgcagggcgacgggcctgggggccgcttaacagcagtagtgtt 2397 
98 to	ccaacctggcagctgttggggacctgttgcactcaagccaggcttcactgacagcc 2457 
58 tt 	tggggttgcggctgcacctgccgggcgcctctcccagggagtggctcttccatcaca 2517 
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78 C1 18 C1	tgogcatecetettecttecagaaceetettecatatggetgeegatggaecaggg 2637 
38 ccc	coccagoaggocatygagggaggagtggccatggtccaccttcctcccatcaccac 2697
38 C – 3	caccaccatcaccatcaccgaggggggagaaccccaggggacactttgccccgttccat 2757 
58 g - 98 G	gctatagcaagagcgaggacctctctacaggggtccctaagccccctgcggcctccatc 2817 
18 c   58 C	cttcacagccacagctacagtgatgagtttggaccctctggtactgattttacccgtcgg 2877 
78 c   18 C	cageteteactteaggacaacetacagcacatgetetececgcccagateaccateggt 2937 
38 c 1 78 C	cccagaggccagctccctcagggccaggagggcagtggtgggggcagtggtgggggc 2997 
98 g - 38 G	9tggggccagccacctcccttgcagagggcaaatctcagcagttgacagtgagtg
58 g - 98 G	cccagaaaccccggccgtccagcgggaacctattgcagtccccggaaccagttatggt 3117 
18 c - 58 C	ttgcccgtccacggcaacagagcctcagcaaagaggcagcattgggggcagcgggggc 3177 
78 a   18 A	geggtggcggaggggtgggggctcaagcctccatcaccaagcattcccagact 3237 
38 c - 78 C	catccacyctgaaccccacyatyccyyctcyyaycyyactytaycctyyytyccaat 3297 
98 at	tgecteaectgteegetgaeategagagtgeaeaeattgagegggaagagtaeaagetg 3357 {

Norway rat. Rattus norvegicus Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 3777 gagatccactcactgaaggaaaggctacacatgtccaaccggaagctggaagatacgag 3477 occcettgggtecaacaaaccgcgtgtgacgetggcccacettggaacggcctggc 3773 4014 ccatctgtcaaccccactgctccattccaggaggagagggggggccctcaggtgcctct 4073 3358 aaggagtactcgaagtccatggacgaggccgactggacagggtgaaggagtacgaggag 3417 3358 GAGATCCACTCACTGAAGGAAAGGCTACACATGTCCAACCGGAAGCTGGAAGAGTACGAG 3417 3478 eggaggetgetgteccaggaagagcagaccagcaagatectgatgcagtaccaagecege 3537 gotgagccgctgcctgaacccaagaagaggctgctcgacgctca----gagaggcagctt 3713 3774 cccccagccccaccccccccccgcccggctgcagatcacagagaacggcgagttccggaac 3833 4074 caccccaggacaccacctacccacacagaccccttcactctggggtgctatccccatcc 4133 4018 CACCCCAGGACACCAACCCCACACAGACCCCTTCACTCTGGGGTGCTATCCCCATCC 4077 3238 ATGCCTCACCTGTCCGCTGACATCGAGAGTGCACATTGAGCGGGAAGAGTACAAGCTG 3297 14-SEP-2000 AF058789 4539 bp mRNA ROLL Rattus norvegicus SynGAP-a mRNA, complete cds. AF058789 1 (bases 1 to 4539) Kim, J.H., Liao,D., Lau,L.F. and Huganir,R.L. AF058789.2 GI:10122137 4078 T 4078 4134 t 4134 DEFINITION ORGANISM 3298 3598 3418 3658 3714 AUTHORS ACCESSION REFERENCE RESULT (AF058789 KEYWORDS VERSION g Вp Ω qq Db qq ò g ò d ōλ pp Qγ qq Óγ g ò ð δλ ò ò ö δλ δ

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VATLAGRHFTEQWYPVTLPTGSGGSGGGGGGGGGGGGGGGGGGGGGGGAVRIKARYQ

WASILPMELYKEPAEVYTHYRMLCANLEPALNYKGKEEVASALUHILOSTGCKAKDFL

SDMAMSEVDRPMERHLIFFRENTLATKAIESYMRLIGGKYLKDAIGEFIRALYESEEN

CEVDPIKCTASSLABEHOANLRNCCELALCKVVNSHCVPPRELKEVFRAWRLRCAERGR

PENDARLISASLFRFLCPAIMSPSLFGLMQEYPDEQTSRTITLIAKVIQNLANFSKF

TSKEDFLGFRNEFLELEWGSMQFLYFISNLOPTHYNSSFESTSTRANFALLM

EVLPQLSKEALIKKEPPRILSTARINNIQNGPSRCARSQPWVLKGPSAEN

GGYMMRDLNSSIDLQSFWARGLNSSMDMARLPSPTKEKPPPPPGGGKDLFYVSRPPL
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="neuronal RasGAP; contains PH domain, C2 domain, GAP domain in the N-terminal region, and a T/SXV \mod i at the
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MEAAPAAPFRPSQGFLSRRLKSSIKRTKSQPKLDRTSSFRQILPRFRSADHDRARLMQ
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RSAAERDKWIENLQRAVKPNKDNSRRVDNVLKLWIIEARELPPKKRYYCELCLDDMLY
ARTTSKPRSASGDTVFWGEHFEFNNLPAVRALRLHLYRDSDKKRKKDKAGYVGLVTVP
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PLFHMAADGPGPPAGHGGSSGHGPPSSHHHHHHHHHHRGGEPPGDTFAPFHGYSKSED
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PHLSADIESAHIEREEYKKLKEYSKAMDESRLDRVKEYEEETHSLKERLHWSNRKLEEY
ERRLLSQEEQTSKITLMOYQARLEOSEKRLRQOQVEKDSQIKSIIGRLMLVEEELRRDH
PAMAEPLPEPKKRLLDAQLLIR"
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                                                                                                                                                                             Submitted (09-APR-1998) Neuroscience, Johns Hopkins Medical Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA On Sep 14, 2000 this sequence version replaced 91:3065888.
SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90
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98.08; Pred. No. 0;
ative 0; Mismatches 1; Indels 83;
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/tissue_type="hippocampus"
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/protein_id="AAC63510.2"
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Kim,J.H. and Huganir,R.L.
Direct Submission
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Q7 Dp		geceggecatcatgtegeceagtetgtttggaetgatgeaggagtaeceagatgagea 167 
Oy Db	1671	gacctcacgaacctcaccctcatcgccaaggttatccagaacctggccaactttccaa 1730 
Oy Db	1731 1869	gtttacctcaaaggaggacttcctgggcttcatgaacgagtttctggagctggagtgggg 1790 
Oy Db	1791 1929	ttctatgcagcaattcttgtatgagatatccaacctggacacactgaccaacagcagcag 1850 
Oy Dp	1851 1989	ttttgaggctacatagacttgggccgcgagctctccacacttcacgccctgctctggga 1910 
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Qy	2211	tocogytggggtaaagacetgttetatgtgagceggceaceaetggcecggtectecec 2270 
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oy Dp	2331	caagagtgtgtccatgctggacctgcagggcgacgggcctgggggccqccttaacagcag 2390 
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Qy Db	2451 2589	agcagcettggggttgcggcctgccgggcgcctctcccaagggagtggctcttc 2510 
à d	2511	catcacagcagcagcatgcgcctcagccagatggtgtcactacggatgtgtccccgc 2570 
QY	2571	gcaactgcgcatccctcttccttccagaaccctctctccatatggctgccgatgg 263

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for endogenous CaMKII; can

p135

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activate intrinsic ras GTPase activity"
/note="synaptic ras GAP; N-terminal encodes putative PH
domain, C2 domain, and ras-GAP domain; C-terminal encodes
proline-rich region, stretch of 10 histidine residues, and
t/SXV motif; enriched in the forebrain postsynaptic
                                                                                                          /product="synaptic ras GTPase-activating protein
           122. .4003
/function="prominent substrate
db_xref="taxon:10116'
                                                                                        density fraction'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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99.9%;
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2 (bases 1 to 4063)
Chen, H.-J., Rojas-Soto, M. and Kennedy, M.B.
A synaptic Ras GrPase-activating protein (pl35 SynGAP) inhibited by Cam Kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                        SogtONO. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Biology, California Institute
a Blvd., MC 216-76, Pasadena, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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AF048976.1 GI:2935447
                                                                                                                 4089 CCTTCCCTGTGCCACCCTACCCCGGCCCAGCGTCACAGACCTCCTTCCCAGTGCACC
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    CGCCATGGCTGAGCCGCTGCCTGAACCCAAGAAGAGGCTGCTCGACGCTCAGCTCCTCAT
                                               Chen, H.-J. and Kennedy, M.B.
Identification and cloning of a novel 130
ras GrPase-activating domain from the rat
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/strain="Sprague-Dawley"
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Rodentia;
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Chen, H.-J. and Rennedy, M.B.
Direct Submission
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Submitted (14.302-1998) to the DDBJ/EMBL/GenBank databases. Tatsuo
Suzuki, Shinshu University School of Medicine, Department of
Neuroplasticity, 3-1-1 Asahi, Matsumoto, Nagano 390-6621, Japan
(E-mail:suzukiteGeth.md.shinshu-u.ac.jp, Tel:+81-263-37-2683,
Pax:+81-263-37-2723,
On Mar 16, 1999 this sequence version replaced gi:4239945.
Sequence updated (09-Reb-1999).
                                                                                                                                      synGAP-bi.
Rattus norvegicus (sub_species:Sprague Dawley) cDNA to mKNA.
Rattus norvegicus.
Bukartyota: Wetaboa Chordata; Craniata: Vertebrata; Euteleostomi;
Bukartyota: Wetaboa Chordata; Craniata: Vertebrata; Euteleostomi;
Wammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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δ	2869	accepteggcageteteactteaggacaacetacagcacatgeteteccegcecagate 29	28
QQ	3824	ACCGTCGGCAGCTCTCACTTCAGGACAACCTACAGCACATGCTCTCCCCGCCCCAGATC 38:	83
Qy Db	2929	accatcggtccccagaggccagctccctcagggccaggaggggacattgggggcagt 29000000000000000000000000000000000000	88 43
Qy	2989	ggtggggggggggggggggggggggggggggggggggg	48
qq	3944	GTGGGGGCGGTGGGGGCCACCTCCCTTGCAGAGGGCAAATCTCAGCAGTTGACA 40	03
Oy Dp	3049	gtgagtgctgcccagaaacccggccgtccagcggggaacctattgcagtccccggaacca 31. 	08 63
ογ	3109	agttatggtcctgcccgtccacggcaacagagcctcagcaaagagggcagcattgggggc 31	89
Q	4064	AGTTATGTTCTCTCCCCCTCCACGCACAGGCCTCAGGCAAAAGGGCCAGCATTGGGGGC 41.	23
δλ	3169	agcggggcagcggtggcggaggggtgggggtcaagcctccatcaccaagcat 32	28
Д	4124	AGCGGGGCCAGCGGTGGCGGAGGGGGGGCTCAAGCCCTCCATCACCAAGCAGCAT 41	83
O.Y	3229	teccagactecatecacgetgaaceceagatgeeggeeteggageggaetgtageetgg 32)	88
2	200	מוסיים ביים ביים ביים ביים ביים ביים ביים	
8 8	24	9 STATEMENT OF THE STAT	
δy	ñ	tacaagctgaaggagtactcgaagtccatggacgagagccgactggacagggtgaaggag 34/ 	
g	Š	TACAAGCTGAAGGAGTACTCGAAGTCCATGGACGAGGCCGACTGGACAGGGAG 43:	
ò	40	tacgaggagagatccactcactgaaggaaaggctacacatgtccaaccggaagctggaa 34º	
qq	35	TACGAGGAGGAGATCCACTCACTGAAGGAAAGGCTACACATGTCCAACCGGAAGCTGGAA 44:	
Οy	3469	gagtacgagcggaggctgctgtcccaggaagagcagaccagcaagatcctgatgcagtac 35	28

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human chromosome of constructed by the Sanger Centre Chromosome of Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chfs compared from overlapping clones. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Emm., EMBL: Sw., SWISSPROT: Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contigs of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSDJ570F3 94770 bp DNA PRI 17-DEC-1999 Human DNA sequence from clone RP4-570F3 on chromosome 6 Contains a gene similar to Ratus norvegicus synaptic ras GTPase-activating protein pl35, the CICK0721Q.5 (polypeptide from patented cDNA Em.E06811) gene, the PHF1 (PHD finger protein 1) gene, the RNSL2 (Kinesin-like 2) gene, the gene for acyl-protein thioesterase, ESTS, GTSS, GSSS and a CPG Island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia! Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 94770)
Mashreghi-Mohammadi,M.
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3636 gcgccgggaccacccgccatggctgagccgtgcctgaacccaagaagaggctgctcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4598 GCGCCGGGACCACCCCGCCATGGCTGAGCCGCTGCACCCAAGAAGAGGCTGCTCGA
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                                                                                                                                  3529 caagcccgcctggagcagagcgagaagcgcttgaggcagcagcaggtggagaaggactcc
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Homo sapiens
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/qene="dJ570F3.1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(1012. .1185,1669. .2740,3135. .3176,
3870. .4048,4255. .4456,4664. .4900,6710. .6854,7066. .7210,
338. .7965,10016. .10114,10324. .10477,12824. .12945,
13378. .13469,19727. .19832,22032. .22153,25299. .25366))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(<1012, .1185,1669, .2740,3135, .3176, 3870, .44048,4255, .4456,4664, .4900,6710, .6854,7066, .7210, 7338, .7961,10016, .10114,10324, .10477,12824, .1245, .13469,19727, .19832,22032, .22153,25299, .25320))
                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP4-570F3 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone RP4-570F3 is at 1 in this sequence. The true left end of clone RP4-570F3 is at 44671 in this sequence. The true left end of clone ICRF6c-CR071Q10 is at 20826 in this sequence. The true left end of clone ICRF6c-CR071Q10 is at 20826 in this sequence. The true right end of clone ICRF6c-CR072LQ is at 61562 in
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RSAAERKHIENLQRAYRKONSKYVOVLGLAILTERRESPEKREYCELCLDDMLY
ARTTSKRPASACDTVFKVGEHPENNLPAVRALKLHIYRDSDFKRKKDKAGYVGLVTVP
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EDIADRLISASLFLRFLCPAIMSPSLFGLMQEYPDEQTSRTLTLTAKVIQNLANFSKF
TSKEDFLGFWNEFLELEWGSMQQFLYEISNLDTLINSSSFEGYIDLGRELSTLHALLM
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DEDEIHPLLIRDRRSESSRNKLLRRTVSVPVBGRPHGEHEYHLGRSRRKSVPGGKQYS
MEGAPAAPFRPSQGFLSRRLKSSIKRTKSQPKLDRTSSFRQILPRFRSADHDRARLMQ
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QGYMMRDLNSSIDLQSFWARGLNSSMDMARLPSPTKEKPPPPPGGGGKDLFYVSRPPL
ARSSPAYCTSSSDITEPEQKMLSVNKSVSMLDLQGDGPGGRLNSSSVSNLAAVGDLLH
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PRQQSLSKEGSIGGSGGGGGGGLKPSTTKQHSQTPSTLNPTMPASERTVAWVSNM
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP4-570F3 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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Em:AB016962 Em:AF050183 Em:AF047711 Em:AF053938"
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Wp:CE23411 Wp:CE23475 Wp:CE23472 Wp:CE23470 Wp:CE23474
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GTase=activating protein pl35 SynGAP)"
complement(1012. 25366)
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GTPase=activating protein pl35 SynGAP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/note="11 copies 3 mer ggt 90 conserved"
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/note="89 copies 2 mer gg 56 conserved"
complement(4211. .4599)

repeat\_region mis@\_feature

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                                                                                                                                                                                                                                                                                                                                                                                 8476. .8841
/hote="MLTIC repeat: matches 109. .461 of consensus"
10989. .11119
                                                                                                                                                                                                                                                                                                          8077. .8178
/note="ML/IC repeat: matches 6. .109 of consensus"
8476. .8841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="78 copies 2 mer cc 57 conserved"
24706. 24831
/note="14 copies 9 mer ctctccct 61 conserved"
25104. 25289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=12 copies 9 mer ctcccccc 64 conserved"
25367. 25465
/note="11 copies 9 mer ggggaggag 69 conserved"
27333. 25522
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28854. .29088)
/qene="cfCK07210.5"
/note="match: cDNAs: Em:AF106943 Em:E06811
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="FLAN_C repeat: matches 3. .131 of 13130. .13161 /note="16 copies 2 mer ca 93 conserved" 1326. .13303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="19 copies 3 mer agg 86 conserved" 26820. .27191
/note="match: GSS: Em:AQ605113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="32 copies 3 mer gcc 63 conserved"
19005. .19078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="37 copies 2 mer ga 67 conserved"
19612. .19691
/note="40 copies 2 mer cc 63 conserved"
19658. .19911
/note="27 copies 2 mer cc 70 conserved"
24653. .24808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="24 copies 2 mer ct 75 conserved"
[7111. ,17815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="72 copies 2 mer cc 63 conserved" 7515. 17658
note="72 copies 2 mer gg 59 conserved"
                                                                                                       /note="3 copies 15 mer 91 conserved" 4903. .4970 /note="34 copies 2 mer ga 70 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="93 copies 2 mer cc 59 conserved"
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                                                  /note="28 copies 2 mer ca 94 conserved"
                                                                                                                                                                                       4996. .5190
/note="13 copies 15 mer 59 conserved"
complement(6393. .6846)
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Anote="6 copies 15 mer 70 conserved"
[7370. .17513
                                                                                                                                                                                                                                            complement(6393, .6846)
/gene="dJ570F3.1"
/note="match: GSS: Em:AQ475907"
'note="match: GSS: Em:B68206"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="CpG island"
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                             .4539
                                                                                  .4649
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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: LOSP52; 100% of reads
Sequencing vector: plasmid: LOSP52; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Consensus quality: 145680 bases at least 0%
Consensus quality: 145680 bases at least 0%
Consensus quality: 148600 bases at least 0%
Insert size: 150756; sum-of-contigs
Insert size: 148326; 10.8% error; agarose-fp
Quality coverage: 6.43x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                             Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequesf@sanger.ac.uk on Sep 9, 2000 this sequence version replaced gi:9796876.
NA HTG 29-SEP-2000
clone RP11-175A4, *** SEQUENCING IN
                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                   tgagtgctgcccagaaacccggccgtccagcgggaacctattgcagtccccggaaccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11: gap of 100 bp 70293: contig of 15582 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54611: contig of 54611 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coveraĝe: 6.54x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 150956: contig of 80563
Location/Qualifiers
1. 150956
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                          Homo sapiens chromosome 6 clone R
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                 AL161903
AL161903.12 GI:10039702
                                                                                                                                                                                                                                                                                                                                 (bases 1 to 150956)
                                                                                                                                                                                                              150956 bp
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54712 70293
70294 70393: 9
70394 150956
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                          code: SC
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AL161903/C
LOCUS
DEFINITION
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TITLE
JOURNAL
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                1904
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                 2744 ACAGCTCTATGGACATGGCTCGCCTCCCCTCCCCACCACCAGGAAAAGCCACCCCCACCAC
                                                                                                                                                                                             acagetetatggacatggetegeeteceetececaaccaaggagaaacceeegeeeee
                                                                                                                                             69; Length 94770;
                                                                                                                                                                      ;
0
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                                                                                                                                       Score 920.8; DB 69;
Pred. No. 1.3e-167;
                                                                                                                                                                       0; Mismatches
                                                                                                                                                 22.3%;
91.0%;
                                                                                                                                                                          Matches 979; Conservative
                                                                                                                                                              Similarity
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                                                                                                                                                              Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  99233 CCTCCATCCTTCATAGCCACAGCTACAGTGATGAGTTTGGACCCTCTGGCACTGACTTCA 99174
                                                                                                                                                                                                                                                                                                                       2210 ctcccggtggggtgaagacctgttctatgtgagccggccaccactggcccggtcctccc 2269
                                                                                                                                                                                                                                                                                                                                                                                                                      2330 acaagagtgtgtccatgctggacctgcagggcgacgggcctgggggccgccttaacagca 2389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagcagcettgggggttgcggcetgcacetgccgggcgceteteccaagggagtggetett 2509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2750 cgttccatggctatagcaagagcgaggacctctctacaggggtccctaagcccctgcgg 2809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaccagggcccccagcaggccatggagggagcagtggccatggtccaccttcctcccatc 2689
                                                                                                                                                                                                                                                                           2150 acagetetatggaeatggetegeeteceetececaaceaaggagaaaceeegeegeeee 2209
                                                                                                                                                                                                                                                     Gaps
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Pred, No. 1.1e-167;
                                                                                                                                                                                                                                                    ;
                                                                                                                                                                               200 others
                                                                                                                                                                                                                                                    97; Indels
                                                                                54712 70293
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70394 150956
/note="assembly_fragment:02844
/ragment_chain:1
clone_end:SP6
                                               /note="assembly_fragment:01454
                                                                                                                                                                  vector_side:right"
37381 c 36411 g 37389 t
                                                                                                                                                                                                                                                   0; Mismatches
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/chromosome="6"
/clone="RP11-175A4"
                                                                     vector_side:left"
                                                                                                                                                                                                                            Query Match 22.3%;
Best Local Similarity 91.0%;
Matches 979; Conservative
                                                          clone_end:T7
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                                     misc_feature
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Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169323)
99173 CCCGTCGGCAGCTTTCACTCCAGGACAACCTGCAGCACATGCTGTCCCCTCCCCCAGATCA 99114
                                                                                         98993 TCAGCGCAGCCCAGAAACCCCGGCCATCCAGCGGAATCTATTGCAGTCCCCAGAGCCAA 98934
                                                                                                                                                                                                                                                                                                                                                                                                                                         tgagtgctgcccagaaaccccggccgtccagcgggaacctattgcagtccccggaaccaa 3109
                                                                                                                                                                          3110 gttatggtcctgcccgtccacggcaacagagcctcagcaaaagaggcagcattgggggca 3169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9212890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L008752; 100% of reads
Sequencing vector: plasmid; L008752; 100% of reads
Consensus quality: 155424 bases at least Q40
Consensus quality: 165003 bases at least Q30
Consensus quality: 165252 bases at least Q30
Insert size: 167023; sum-of-contigs
Insert size: 186175; 5.7% error; agarose-fp
Quality coverage: 3.59x in Q20 bases; sum-of-contigs Quality
coverage: 3.22x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3170 gcgggggcagcggtggcggaggggggtgggggctcaagccttcatcaccaagcag 3225
                                                       2930 ccatcggtccccagaggccagctcctcagggccaggagggggagggcagtg
                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5457 5556; gap of 100 bp 5557 876: contig of 3211 bp in length 8768 8867: gap of 100 bp
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Homo sapiens chromosome 6 clone RP11-567N9,
PROGRESS ***, 24 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
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HTG; HTGS_PHASE1; HTGS_DRAFT
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99355 99444: gap of 100 bp 11 length 111056 111155: contig of 11601 bp in length 111156 111155: contig of 11601 bp in length 111156 111155: contig of 7490 bp in length 11846 118745: gap of 100 bp 1846 122421: contig of 3676 bp in length 12242 122521: gap of 100 bp 12222 132468: contig of 5391 bp in length 132569 132568: gap of 100 bp 132569: contig of 5391 bp in length 132569 137959: contig of 5391 bp in length 137950 138059: gap of 100 bp 13059 13059: contig of 13632 bp in length 151692 151791: gap of 100 bp 158231: contig of 6452 bp in length 158354 158353: contig of 100 bp 169351: contig of 100 bp 169351: contig of 100 bp 169351: gap of 100 bp 169351: contig of 1000 bp
                                                                                                      26592 26691: gap of 100 bp 26692 31188: contig of 4497 bp in length 31289 31289: gap of 100 bp 31289 37579: contig of 6291 bp in length 37580 37679: gap of 100 bp 37680 45350; contig of 7671 bp in length 45351 45450: gap of 100 bp 45451 48354: contig of 2904 bp in length
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8868 17168: contig of 8301 bp in length
17169 17268: gap of 100 bp
17269 26591: contig of 9323 bp in length
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83307: contig of 2543 bp in length
83407: gap of 100 bp
88383: contig of 4976 bp in length
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/db_xref="taxon:9606"
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158354, 116932, 169323
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41332 c 41269 g 42673 t 2:
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1 (bases 1 to 829)
Chen,H.-J. and Kennedy,M.B.
Identification and cloning of a novel 130 kd protein containing a
ras GTPase-activating domain from the rat forebrain postsynaptic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                             ccatcacagcagccggcatgcgcctcagccagatgggtgtcactacggatggtgtccccg 2569
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Rattus norvegicus p135 SynGAP mRNA, partial cds.
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/translation="MGLRPPTPSGGSGSGSLPPPSHRQPLRRRCSSCCFPGEFHLG
RSRRKSVPGGRQYSWEAAPAAPFRPSQGFLSRRLKSSIKRTKOPKLDRTSSFRQILP
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266 c 218 g 163 t
Chen, H.J., Rojas-Soto, M., Oguni, A. and Kennedy, M.B.
A synaptic Ras-GTPase activating protein (p135 SynGAP) inhibited by
Cam Kinase II
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//note="synaptic ras GTPase-activating protein; N-terminal
spilce variant; synaptic ras-GAP"
/codon_start=1
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                                                                                                                                 Submitted (16-MAR-1998) Biology, California Institute of Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA
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Pred. No. 5.6e-111;
0; Mismatches 0;
                                                                                                                                                                                                               /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
183: .>829
                                                                                                                                                                                                                                                                                                                                   /product="p135 syngAP"
/protein_id="AAC23491.1"
/db_xref="G1:3213254"
                                             Neuron 20 (5), 895-904 (1998)
98282016
                                                                                                                                                                                     Location/Qualifiers
                                                                                                  Kennedy, M.B.
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Chen, H.-J. and Kenn
Direct Submission
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CCAGGATTCTTCAGCAAGCGCCTGAAAGGCTCCATCAAGAGGACCAAAAGCCAGTCAAAG 302

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A novel human RasGAP-like gene that maps within the prostate cancer susceptibility locus at chromosome 1q25 FEBS Lett. 441 (1), 127-131 (1998) 99093006
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LVTILOSTGRANDFLTDLWEVDROCCEBHOLLFRENTATAKSTEET KLUVGQOYLHD
ALGEFTKALVESDENCEVDPSKCSSELIDHGSNLKMCCELAFCKIINSYCVPPRELK
EVFASWKQQCLNRGKQDISERLISASLFLRFLCPAIMSPSLFNLMQEYPDDRTSRTLT
LTAKVQLANARAKFGNREEYMARNDFLHRRGGMKRFLLEISNPDTISNTPOFDGY
LDGREELSLANGSLUSKGBNSFLQATVAKLGFLPRVLADITKSLTUPPIQO
OLRRFTEHNSSPNVSGSLSGLQKIFFDFLHKLKSPSQDNTDSYFRGKTLLLUVQ
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SIDSSLENLSTASSRSQSNSEDFKLSGPSNSSMEDPTKRSTQSEDFSRRHTVPDRHIP
LALPRONSTGQAQIRKVDQGGLGARAKAPPSLPHSASLRSTGSMSVVSAALVAEPVON
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VEFTEQULDEAKHARKY ROBITKKLREALRAVSRSRLEEV ERRLLVQVEGOMQKLLLEYKA
RLEDSEERLRRQDEEKDSQMK SIISRLMAVEELKKDHABWQAVIDAKOKIIDAQEKR
IVSLDSANTRLMSALTQVKERYSMQVRNGISPTNPTKLSITENGEFKNSSCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noto,S., Maeda,T., Hattori,S., Inazawa,J., Imamura,M., Asaka,M. and
Hatakeyama,M.
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KDNCRRAENVLRLMIIEAKDLAPKKKYFCELCLDDTLFARTTSKTKADNIFWGEHFEF
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Direct Submission
Submitted (11-FEB-1998) Department of Viral Oncology, The Cancer
Institute, Japanese Foundation for Cancer Research, 1-37-1
Kami-Ikebukuro, Toshima-ku, Tokyo, Japan
729 TGGATTGAGAATCTACAGAGGGCTGTGAAACCCAACAAGGACAACAGCCGCCGGGTAGAT 788
                                                                                                                                                                                                                             14-JAN-1999
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1 (bases 1 to 4368)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="G1:4105589"
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                            303 CTTGACAGAAACACGAGCTTTCG-----GCTTCCATCCCTTCGCAGTACAGATGAC
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                                                        egggcccggctgatgcagagcttcaaggagtctcactcccatgagtccctgctgagtccc
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15.2%; Score 627.8; DB 10; Length 4368; ilarity 62.4%; Pred. No. 6.1e-111; Conservative 0; Mismatches 572; Indels 78;

Best Local Similarity Matches 1079; Conserv

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (2000) In press
2 (bases 1 to 4287)
0hara-O., Nagase,T., Kikuno,R. and Okumura,K.
Direct Submission
Submitted (24-AUG-2000) to the DDBJ/EMBL/GenBank databases. Osamohara, Kazusa DNA Research Institute, Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence of a long cDNA clone isolated from human
                                                                                                     1465 gecetgigeaaaggiggicaacicecaiigegigiiteeegaagggageigaaggaggigiii 1524
                                                                                                                                                                             1525 gcatcatggcggctgcgctgtgcagagcggggccgggaggacattgctgacaggctgatc 1584
                                                                                                                                                                                                                                                                    1485 GCATCATGGAAGCAGCAGTGCCTGAACCGTGGCAAGCAACATCAGCGAGGGCTCATC 1544
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                                                                                                                                                                                                                                                                                                                                1645 ctgatgcaggagtacccagatgagcagacctcacgacctcaccctcatcgccaaggtt 1704
                                                                                                                                                                                                                                                                                                                                                                                                           1705 atccagaacctggccaacttttccaagtttacctcaaaggaggacttcctgggcttcatg 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1665 ATTCAGAACCTGGCCAACTTTGCCAAGTTTGGTAACAAAGAGGAATACATGGCATTCATG 1724
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                                                                           1405 aagtgcacagcgtccagtctggcagagcaccaggccaacctgcggatgtgctgtgagttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fis (full insert sequence). Homo sapiens adult spleen cDNA to mRNA, clone:as000087 \,
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Homo sapiens mRNA for FLJ00087 protein, partial cds.
AKO24488
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/translation="GSTLHLRCLLWGANKPKRFPPSHSHLQDNVEREETWLSVWVHBA
KGPPRAAGAGRGVRAELWLDGALLARTPPRAGPGOLRWAERTERBALPRELSLRLR
GLGPGSAVLGRVALALEELDARRAPAAGLERWRPLLGAPAGAALRARTRARTREVLPS
BRYKELAEFLTFHYARLCGALEPALPAQAKEELAAAMVRVLRATGRAQALVTDLGTAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARCGGREALLFRENTLATRAIDEYMKLVAQDYLQETLGQVVRRLCASTEDCEVDPSK
CPASELPEHQARLRNSCEEVFETITHSYDWFPAELGIVFSSWREACKERGSEVLGPRL
VCASLFLRLLCPAILAPSLFGLAPDHPAPGPARTLTLIAKVIQNLANRAPFGEKEAYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFMNSFLEEHGPAMQCFLDQVAMVDVDAAPSGYQGSGDLALQLAVLHAQLCTIFAELD
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                                                                                                                                                                                                                                                                                                                                                                  Jobe-"For this clone, GeneMark analysis triggered an alert for spurious CDS split. The result of GeneMark analysis of the nucleotide sequence of this clone is accessible through http://www.kazusa.or.jp/NEDO. Start codon is not identified."
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1529 c 1261 g 712 t
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Pred. No. 6.4e-55;
0; Mismatches 396; Indels 0;
                                                                                                                                                 /tissue_type="spleen"
/note="vector:pBluescript11 SK plus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"FLJ00087 protein"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="as00087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB15778.1"
/db_xref="G1:10440490"
                                                                                                          /dev_stage="adult"
                                                                                                                                                                                                                    1339. .3363
/gene="FLJ00087"
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AC019800 56366 bp DNA HTG 03-JAN-2000 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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                                         1550 agoggggcogggaggacattgctgacaggctgatcagcgcctcgctcttcctgccttcc 1609
                                                                                                                                                                                                                                                                                                 1730 agtttacctcaaaggaggacttcctgggcttcatgaacgagtttctggagctggagtggg 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1850 gittigagggetacatagacitgggeegegageteteeacaciteaegeeetgeteiggg 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2609 GTTACCAGGGCAGTGGTGATCTGGCCCTCCAGTTAGCTGTCCTGCATGCCCAGCTCTGTA 2668
2249 ACGACTGGTTCCCTGCGGAGCTGGGCATCGTGTTCTCAAGCTGGCGAGAAGCATGTAAAG 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was identified as CDM:10210991 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                   2369 TGTGCCCTGCCATCCTGGCACCCAGCCTTTTGCTTTGCACCAGACCATCCAGCACCCG
                                                                                                                                                                                                                                     2429 GCCCAGCCCGCACCTCACACTGCCAAGGTCATCCAGAACCTCGCCAACCGTGCCC
                                                                                                                                                                                                                                                                                                                                        2489 CGTTCGGTGAGAAGGAGGCCTACATGGGCTTCATGAATAGCTTCCTGGAGGAACATGGAC
                                                                                                                                                                                                              1670 agaceteacgaacceteaceeteategecaaggttatecagaacetggecaactttteea
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                                                                                                                                                                                                                                                                                                                                                                                                                           2549 CAGCCATGCAATGCTTCCTGGACCAGGTAGCCATGGTGGATGTGGATGCTGCCCCCAGTG
                                                                                  2309 AACGTGGCTCTGAGGTGCTGGGCCCCCGACTGGTGTGCGCCTCCTCTTCCTGCGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.8%; Score 241.8; DB 39; Length 56366; 50.6%; Pred. No. 5e-37; tive 0; Mismatches 682; Indels 48;
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 56366)
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/db_xref="taxon:7227"
11924 c 11808 g 16400 t
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1. .56366
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HTG; HTGS_PHASE2.
fruit fly.
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Direct Submission
Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
CA For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence) or send email
to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.
* NOTE: This is a "working draft' sequence. It currently
* consists of 142 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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RPCI-98 01.N.10 map 16D-16F strain Y; cn bw sp, *** SEQUENCING IN
PROGRESS ***, 142 unordered pieces.
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Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                 Score 241.8; DB 36; Length
Pred. No. 3.6e-37;
0; Mismatches 682; Indels
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Drosophila melanogaster chromosome X clone BACR01122 (01114)
RPCI-98 01.1.22 map 16B-16D strain y; cn bw sp, *** SEQUENCING IN
PROGRESS ***, 142 unordered pieces.
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                                                       Db 114309 TICGAATCGCACAAGCATTITCCCGCCCAGTTACGAAATGCTTTGCGACGTTCCGGGAG 114368
                                                                                                                                                                                                                                                                                    Db 114369 CGCTTGCAGCAGCTGGGCCGTCAGGATATGGCCGACAACCTGATCTCGGCGAGCATTTTC 114428
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                                                                                                                 1480 gtcaactcccattgcgtgttcccgagggagctgaaggaggtgtttgcatcatggcggctg 1539
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Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 20141)
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Under Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley, Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley, CA 94720, USA CON NO 16, 1999 this sequence version replaced 91:6425635. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a "working draft' sequence record is consists of 142 contigs. The two order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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                                      Rubin, G.M.
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Db 126449 GAGCGCGACTTTGGATCTACTCGCTGCGCAAGTCGATCGCTCCGAATGCAGAGCACGG 126390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%; Score 241.8; DB 36; Length Best Local Similarity 50.6%; Pred. No. 3.5e-37; Matches 749; Conservative 0; Mismatches 682; Indels
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Drosophila melanogaster genomic scaffold 142000013386053 section 23 of 30, complete sequence.
AE003506 AE002593
AE003506.1 GI:7293355
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                                                                                                                                                                                            Db 125756 GATCAGAGG---CTTACGTTCAGGGGCAACTCCTTGGCCACCAAGAGCATGGAGGCATTC 125700
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                               Oy 1420 agtetggcagagcaccaggccaacctgcggatgtgctgtgagttggccctgtgcaaggtg 1479
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1 (bases 1 to 300944)
Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,
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REFERENCE

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Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., Gorge, A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Melt, G., Champe, M., Ffeiffer, B.D., Wan, K.H., Doyle, C.C., Barter, E.G., Helt, G., Nelson, C.R., Gabor, Miklos, G.L., Abril, J.F., Agbayani, A., An. H.J., Beson, R.Y., Benos, P.V., Berman, B.P., Bhadari, D., Ballew, R.M., Basu, A., Benos, P.V., Berman, B.P., Bhadari, D., Bolshakov, S., Borkova, D., Bustoha, M.R., Bouck, J., Brokstein, P., Brottler, P., Burtis, K.C., Bushor, J.M., Cadleu, E., Corter, A., Chandra, I.C., Cherry, J.M., Candey, S., Marker, D. Busam, D.A., Buller, M., Cadleu, E., Corter, A., Chandra, I.C., Busam, D.A., Buller, M., Daylar-Rocha, S., Dunkov, B.C., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Ferleschmann, W., Fosler, C., Gabriellan, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Gelbart, W.M., Glasser, M., Brith, D., Heiman, T.J., Herrandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Hernandez, J.R., Houck, J., Hostin, D., Holls, M., Marris, M., Marris, M., Marris, M., Marris, M., Marris, M., Morleo, M., Murphy, B., Murphy, L., McLeod, M., Nelson, D.L., Nelson, D.L., Nelson, D.K., Markei, B., Murphy, B., Murphy, L., Musskern, D. R., Pacleb, M., Pherson, D.K., Pacle, T., Lin, X., Liu, X., Li
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
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1. .300994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
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REFERENCE
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PDVSGEGPPFRAPTKQELVEFRKQIEGGHIDRVKRIIWENPRFLISSGDTPTSLKEGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGRRULESPILAGE STATESPER PERVINDENCE CERRINDING PULEFPATPITIKKINEDLE MAYRINDSFDERLAGDSQULDMSLSRSLINDSCREEKTEKTDIEFPATPITIKKINEDLE MAYRINDSFDSPLADDSQULDMSLSRSLINDSCREEKTEKTDIERGLEVWORPQLENGE MAYRINDSFDSPLAGTERLESPERGADAGSETVWNFALLHQYFDSMAGEQOQQULRKDRRAGAGSPSPAGVWTPYTCVBKSLQYFAKRITKTLINKIGNWYSINDTLLCELKRLKSLIVSFRDDARFISVDFSKVHSRIAHLVASYVTHSQEVSVAMRLOLLQHLKSLRQLLADBRGREGHLGCVGASLLLMLEQAPTSAVHLDDTKTEELCCAAWETEQCCACLWDANLSRKTSRRKTKSLRAAVVQSQGQLQDTSGSTGSSALHSELCCAAWSTSCASVANRRQQSDBEDYDSDEQVIFFDCTNVTLPYGSSSEDERNFKTPPQSCSSGSSEDENFRTPPQSLSPGTSSALHSTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APVTPRLARTPSAASIQVASETNGESVGTAVTPASPILSFAALTAATQSFQTPLNKVR
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KLCKONPPPFYRPIRVPWCSIKDFOCLDERKSHITHXIROLGGELSGRYTVFNIDKLI
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YFTLRACCMVYKNRQELYEIEBKIRQEPPPKIDLKLSLKSHNPRIGDTPTSAVLKVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSCAEMNLNVKVOKPEPWYSGTSSSHNSOPLLHPKRLLATPKLNAVVSGRRGSGPLT
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25191. 25370,27861. 28115,28453. 28555))
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Y I AESGRP I GEKFMWFCFTS I GAVTALVI I MSLWEKFQTNPTI TGLDTDFHNQNVVFP
                                                                                                       FKSTPTEDVKTGAPHDLYETDKKWALFFIPNSTSRIFIFSNEEYFGSDFNAQIDWSEP
                                                                                                                                                                                                                                                                                  AEESAGPNPLGGYQRKHEKDYSLNTKNYYKTPKVVPDYGYTSKTKNSWTTYDHSQYMP
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CDS

CDS

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PPQSLSPGISMDLEPRYELFIFGNEPTRRDLDVLNALSNVDIDKETLPHVYAWKTAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSGFIIPLGSNSSMSNLLLSDSPTSSPSSSNVIANGRQQMQQQQQQQQQQQQQPQGPVSGB
GPPFRAFTKQELVEFRKQIEGGHIDWYKRIINBENFRLISSOFPTSLKEGCKYNAMH
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PDVSGEGPPFRAPTKQELVEFRKQIEGGHIDRVKRIIWENPRFLISSGDTPTSLKEGC
RYNAMICAQVNRARIAQLILKTISDREFTQLYVGKKGSGKMCAALNISLLDYYLINMP
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GPMSREKAMNFYRRWKTPPRVSNNVMSPLAGSPFSSFVKVTPSKSIFDRSAGNSSPVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGRRVLFSPLAEATSSPKPTKNVPNGTNECEHNNNVKPVYPLEFPATPIRKMKPDLF
MAYRNNNSFDSPSLADDSQILDMSLSRSLNASLNDSFRERHIKNTDIEKGLEVVGRQL
ARQEQLEWREYWDFLDSFLDIGTTEGLARLEAYFLEKTEQQADKSETVWNFAHLHQYF
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                                                                                                                                                                               VASGSPSGSAASVQTGNADDGSAATKYEDPDYPPDSPLWLIFTEKSKALDILRHYKEA
RLREFPNLEQAESYVQFGFESIEALKRFCKAKPESKPIPIISGSGXKSSPTSTDNSCS
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22257. .22823,22889. .23887,24168. .24320,24398. .25116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DD 196157 GAGCGCGACCTTTGGATCTACTCGCTGCGCAAACTCGAATGCAGAGGCACACACG 196216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 196217 CGTCGCACGGACAACTCGCTGAAGATGTGGGTGTACGAGGCGAAAAATCTGCCGCCCAAG 196276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 196277 AAGCGTTACTTTTGCGAACTGCAATTGGACAAGACGCTGTACGGCCGGACTTCGGTGAAG 196336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 196337 CTGCAGAC-----GGATCTGCTGTTTGGGGGGAGCACTTCGATTTCCCCGACATA 196387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 196508 CCCTGCGAACAATGGTATCCCATA--------CTGAGCGACAAGACGGGGGC 196549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 196388 CCCGAGATTAATGTGATCACTGTTAACGTTTTCCGTGAGGTGGACAAGAAGAAGAAGCGG 196447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 196448 GACAAATACCAATTTGTGGGATCGGTGAAGATACCCGTGCACGATGTCACCTCCAGATTG 196507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  889 ttcacagagcagtggtaccccgtgaccctgccaacaggaagtgggggctctgggggtatg 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaaagggacaaatggattgagaatctacagagggctgtgaaacccaacaaggacaacagc 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccccgctcagcctcaggagacactgtcttttgggggcgagcacttcgagtttaacaacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgccgggtagataacgtgctgaaactatggatcatagaagctcgagagctgcccccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagcgatattactgcgagttatgcctggacgacatgctctatgcacggaccacttccaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cctgctgtccgggcgctgcggctgcatctgtaccgtgactcggacaaaaagcggaagaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 28; Length 300994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 241.8; DB 28; Length 50.6%; Pred. No. 3.2e-37; Live 0; Mismatches 682; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="CG8465 gene product [alt 3]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CG8465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649
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197567 GATCCGTTGCAGCATATTCTCGATGAAATCAGCCGAGCC 197605

Search completed: January 18, 2001, 07:18:54 Job time: 20645 sec

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January 18, 2001, 11:15:27; Search time 231 Seconds (without alignments) 2884.142 Million cell updates/sec
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Sequence 3, Appli
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Sequence 15, Appl
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-22-463-14

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US-07-885-971-15

US-07-885-971-15

US-07-885-971-15

US-08-194-087-15

US-08-194-087-16

US-08-194-087-16

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Length 3117;
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APPLICANT: Hiang, Betty
APPLICANT: Hang, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.5%; Score 62; DB 3; Length 311 Best Local Similarity 49.7%; Pred. No. 1.7e-05; Matches 158; Conservative 0; Mismatches 160; Indels
                                                              3677 ccaagaagaggctgctcgacgctcagaggcagc 3711
                                                                                                     1076 RRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGC 1042
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Allen, Maxine J.
APPLICANT: BALCKLer, Alan J.
TITLE OF INVENTION: GAP12 Genes and their Uses
FILE REFERENCE: SEQ-11P
CURRENT APPLICATION NUMBER: US/08/909, 954A
CURRENT FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                             ; Sequence 3, Application US/08909954A; Patent No. 6100058
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US-08-909-954-3
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Best Local Similarity 3.3%; Pred. No. 1.1e-up;
Batches 13; Conservative 233; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30472/114 IMMU
                                                                                                                                                                                             :: Foley & Lardner
1800 Diagonal Road, Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-NG-1991
ATTORNEY-AGENT INFORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                              STALL.
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
TWPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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| 123 | em estpli; * |
| 124 | em estpli; * |
| 125 | em estpli; * |
| 126 | eb estp; * |
| 127 | eb estp; * |
| 128 | eb estp; * |
| 129 | eb estp; * |
| 129 | eb estp; * |
| 120 | eb estp; * |
| 121 | em estpli; * |
| 121 | em estpii; * |
| 122 | em estpii; * |
| 123 | em estpii; * |
| 124 | eb estp; * |
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| 127 | eb estp; * |
| 128 | eb estp; * |
| 129 | eb estp; * |
| 120 | eb estp; * |
| 120 | eb estp; * |
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190: gb\_gss25:\*
191: gb\_gss26:\*
192: gb\_gss27:\*
193: gb\_gss27:\*
No. is the number of results predicted by

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	808002V4 808002V4	200321 1M0164	779747 hnR5f10	53433 hw23d06	9010 zf94h11.	227 fi94f10.	93964 RPCI-2:	6711 ml58d	327	547	œ.	923	5645	4612	3541	3015 RC1-FT	109245	331 wa18	311 fj	UI-R-	:IT978SK	UI-H	tw91e09.	L215753 Tetrao	AA554056 n101g07.s	158d01.r	mp74c11.	Tetraod	UI-H-B11	97 tk62h05	TOTANS.	BEU159/8 IK6ZBU5.Y	111-0-1	97 mp74c11	427 halse10	48 nm56e05.s	3198 192621	874961 ul27f03	084 AJ39908	5114 CM2-BT	7382	72027	AL235430 Tetraodon	95651 MR1-BT0
DB ID	VA	100574 10	AW7797	OR RE4634	AA709	0 AW42122	3 AQ9939	2 AI60671	0 AA691	8 AJ39654	7 AI958829	08 BE4909	11 BE69564	AW204612	36 BE848	35 BE77301	3 AW6567	3 AI6503	9 AW0769	2 AI57756	83 B68206	AW20598	2 AI60960	91 CNS0	9 AA554056	AA107246	9 AI327335	92 CNS04D	0 AW1361	5 AW82649	AA554U55	133 BEU159/8	ALTOCAL 1	AA11839	AFPRAG C	9 AA575948	11 BE723	6 AIB7496	8 AJ39908	34 BE0851	0	191 CNS01XQ5	191 CNS03ANH	1 BE695
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## ALIGNMENTS

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                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                       Bovidae; Bovinae; Bos.
1 (bases 1 to 571)
Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1325 agaaatacctcaaggatgccattggggagttcatccgggctctgtatgaatctgaggaga 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 TGCGGATGTGCTGTGAGTTGGCCCTGTGCAAGGTGGTCAACTCCCATTGCGTGTTCCCGA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 GCAAGGAGGAGGTCGCCAGTGCTCGTTGCAGAGTACAGGCAAGGCCAAGG 70
                                                                                                                                                                                                                                                                                Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kazusugi@cocoa.ocn.ne.jp Single pass sequencing. This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.9%; Score 490.4; DB 37; Length 571; 93.2%; Pred. No. 2e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Bos taurus brain fetus"
/tissue_type="brain"
/dev_stage="fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="ElBR014B04"
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Unpublished (2000)
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(http://www.jax.ources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWMD42 (gil47321414gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 474)
                                                                                                                                                                                                                      A2399131 474 bp DNA GSS 03-OCT-2000
1M0164P14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0164P14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib≈"Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah
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Unpublished (2000)
Contact: Robert B. Weiss
A2399131.1 GI:10514203
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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QQ δλ g ò QQ 9 g δ g Q g δ

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Unpublished (1997)
Context: Robert Strausberg, Ph.D.
Tel: (301) 466-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                             178 9
                                                                                                                                                                        Fatima Bonaldo.
169 c 17
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Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Tel: (301) 496-1550
Tel: (301) 496-150
Tel: (301) 49
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/clone="IMAGE:3034699"
/clone_11b="NOI_CGAP_Kid11"
/lab_nost="DH10B"
/note="Organ: kidney: Vector: pH7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW779747 593 bp mRNA EST 12-MAY-2000 hn85f10.x1 NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:3034699 3' similar to TR:095174 095174 NGAP.; mRNA sequence. AW779747 GI:7794350
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 593)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                             695
                                                                                                                                               755
                                                                                                                                                                                                                                                                                        307 AACCACCTCCAAGCCCCGCTCGGCTTCAGGAGACACCGTCTTTTGGGGCGGAGCACTTTGA 248
                                                                                                                                                                                                                                                                                                                                                                            576 caaggacaacagccgccgggtagataacgtgctgaaactatggatcatagaagctcgaga 635
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                                                                                                                                                                                                                             696 gaccacttccaagccccgctcagcctcaggagacactgtctttgggggggagcacttcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               636 gctgcccccaagaagcgatattactgcgagttatgcctggacgacatgctctatgcacg
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Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneiDs 1322376-1323911, 1456007-1456775, and 150655-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                994 gggaaaggaggctgtcctgctgtgcggctgaaggcccgttaccagacaatgagtatcctg 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054 occatggagetatataaggagtttgcagaatatgtgaccaaccactaccgcatgctgtgt 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 GGCAAGGGCACTGGACCCATGATCAGCATCAAGGCGCGCTACCAAACCATCACCATCCTG 459
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                                                                                                                                                                                                                                                                                                                                                                         Score 294.6; DB 95; Length
Pred. No. 6.3e-58;
0; Mismatches 140; Indels
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source
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             Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
info@image.llnl.gov
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                        /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCK-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1455775, and 150552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 cctggagotcaacctggatgaagactccattatcaagccagtacacagetccatcctggg 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 gagettcaaggagtetcaeteecatgagteeetgetgagteeeageagtgetgetgetgagge 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 250.4; DB 1
Pred. No. 1.1e-47;
                                                                                                                                                                                                                                                              /clone="IMAGE:3183755"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH108"
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                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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147 c 13
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zf94h11.s1 Soares\_pineal\_gland\_N3HPG Homo sapiens cDNA clone IMAGE:384645 3' similar to WP:C07B5.1 CE00891 GTPASE-ACTIVATING PROTEIN ;, mRNA sequence.

24-DEC-1997

EST

427 bp

AA709010

LOCUS

AA709010/c

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1 (bases 1 to 427)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylle,T., Waterston,R. and Wilson,R.
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE CONSORTium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 424.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 TCCTGACAGACCTGATGATGTCAGAGGTGGACCGCTGCGGGGACAACGAGCACCTCATCT 245
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                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
TEL: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:1292902"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:384645"
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118 c 127 g
                    AA709010.1 GI:2718928
                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Wilson RK
                                                                                           Homo sapiens
AA709010
                                                                  human.
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ccgggcccggctgatgcagagcttcaaggagtctcactcccatgagtccctgctgagtcc 383
       264 actigaccogoaccogcostiticoacagatectgeetegeticegaagigetigaecaiga 323
                                                                                                                                          481 CAGGICACGAGGCCTGCCCAAATTGAAGGAGTCCTGTTCCCATGAGTCTTTGCTGAGTCC 422
                                                                                                                                                                                       384 cagcagtgctgctgaggccctggagctcaacctggatgaagactccattatcaagccagt 443
                                                                                                                                                                                                                                   421 TGGCAGCGCTGTTGAAGCTCTGGATCTGAGTATGGAGGAGGATGTCTACATCAAACCTTT
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AQ993964
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1 (bases 1 to 597)
Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, K., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com
) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
?i
                                                                                                                                                                                                                                                  AW421227 597 bp mRNA EST 09-FEB-2000 fj94f10.xl zebrafish gridded kidney Danio rerio cDNA 3' similar to TR:095174 095174 NGAP.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: kidney; Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; Oligo dT cDNA library constructed from mRNA pooled from pooled kidney tissue from 300 adult
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 gcaaggettectgageeggaggetaaaaageteeateaaagteaaagteacaa 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.7%; Score 233.6; DB 90; Length 597;
Best Local Similarity 64.1%; Pred. No. 9.4e-44;
Matches 391; Conservative 0; Mismatches 204; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterstand Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
Other_ESTs: fj94fl0, y1
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1800
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="zebrafish gridded kidney"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: polyT not found
Seq primer: T7 ET from Amersham
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Location/Qualifiers
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/db_xref="taxon:7955"
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Contact: Shaying 2hao
Contact: Shaying 2hao
Contact: Shaying 2hao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
772 Medical Center Dr., Rockville, MD 20850, USA
772 Medical Center Dr., Rockville, MD 20850, USA
773 Medical Center Dr., Rockville, MD 20850, USA
774 Medical Center Dr., Rockville, MD 20850, USA
775 MD 20850,
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RPCI-23-241C10.TV RPCI-23 Mus musculus genomic clone RPCI-23-241C10
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
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Bukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
1 (bases 1 to 682)
564 tgtgaaacccaacaaggacaacagccgccgggtagataacgtgctgaaactatggatcat 623
                                                                                                                                                                                                                                                                                                504 atgittigccigicggicigagccgaaagggacaaaitggatigagatciacagagggc 563
                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TGTGCAACCTAATAAGGACAATTGCCGGGGGGGGGAAAACGTCCTCCGCCTGTGGATCAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  624 agaagctcgagagctgcccccaagaagcgatattactgcgagttatgcctggacgacat 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TGAGGCAAAAGACCTGCCACCAAAAAAAAATATTCTGTGAGCTGTGTCTGGATGACAT 122
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Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies).

190 c 146 g 176 t lothers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 566)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        636 getgecececaagaagegatattactgegagttatgeetggaegacatgetetatgeaeg 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           696 gaccacttccaagccccgctcagcctcaggagacactgtcttttgggggcgagcacttcga 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington Est Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 228.8; DB 173; Length 682; Similarity 91.3%; Pred. No. 1.3e-42; Conservative 0; Mismatches 23; Indels 0;
                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/d_xref="taxon:10090"
/clone="RRCI-23-241110"
/clone_lib="RPCI-23"
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                                   Location/Qualifiers
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/lab_host="DH10B"
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                 Class: BAC ends.
 Seq primer: T7
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This clone is available royalty-free through LLNL; confuct the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vt05d01.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1162177 5' similar to WP:C07B5.1 CE00891 GTPASE-ACTIVATING
PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1110 gtgtgccgtgctggagcccgcctcaatgtcaagggcaaggaggaggaggtcgctagtgcact 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1349 gggagttcatccgggctctgtatgaatctgaggagaactgtgaagtagaccccatcaagt 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              990 caaagggaaaggaggctgtcctgctgtgcggctgaaggcccgttaccagacaatgagtat 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1170 ggttcacatcctgcaaagcacaggca-aggccaaggacttcctttcagacatggccatgt 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1229 cagaggtagaccggttcatggagcgggaacacctcatattccgcgagaacacgctcgcca 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1289 ctaaaagccatagaagagtatatgagactgattggccagaaatacctcaaggatgccattg 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1050 cotgoccatggagotatataaggagtttgcagaatatgtgaccaaccactaccgcatgct 1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 GTGTTCTGTTCTTGAGCCAGTAATTAGTGTGAGGAATAAAGAGGAGTTGGCCTTGTGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 CAGAGGTAGATCGTTGTGGAGAACATGATGTCTTGATCTTCAGAGAAAACACCATTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                               1.566
/organism="Mus musculus"
/organism="Inbred CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:316193"
/sex="males"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.4%; Score 222; DB 22; Length 566; 69.2%; Pred. No. 4.6e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /Lissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
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                                                                                                           correct orientation)
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Best Local Similarity
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1858 ggctacatagacttgggccgcgagctctccacacttcacgccctgctctgggaggtgctg 1917
                                                   313 GGCTACATAGACCTGGGCCGGGGAGCTCTCTAGCCTGCACTCCCTGCTCTGGGAAGCTGTC 372
                                                                                                                      1918 ccccagctcagcaaggaagccctcctgaagctgggcccgct 1958
                                                                                                                                                373 AGCCAGCTTGATCAGAGCGTTGTGTCGAAGCTGGGACCTCT 413

    .707
    /organism="Gallus gallus"

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/clone_lib="dkfz426"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Buerstedde JM
                                                                                                                                                                                                                                                                                                                                                          AJ396547.1 GI:7128594
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Matches 337; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus
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                                                                                                                                                           1 (bases 1 to 413)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., La,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:628089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1558 egggaggacattgctgacaggctgatcagcctcgctcttcctgcgctctctcgccg 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1678 cgaacctcaccctcatcgccaaggttatccagaacctggccaactttccaagtttacc 1737
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                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra MyMouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: -28m13 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                       Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1162177"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                       AA691827.1 GI:2692765
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                     house mouse.
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AA691827
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ORIGIN
ACCESSION
                         VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                      TITLE
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AJ396547 707 bp mRNA EST 03-MAY-2000
AJ396547 dkfz426 Gallus gallus cDNA clone 2601511, mRNA sequence.
AJ396547
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A large database of chicken bursal ESTs as a resource of analysis of vertebrate gene function Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 707)
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237 c 218 g 124 t
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1 (bases 1 to 628)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
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Xenopus laevis
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1 (bases 1 to 555)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Wucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., and Wilson,R., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1958829 555 bp mRNA EST 20-AUG-1999 fd22g01.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR:017774 Q17774 C07B5.l;, mRNA sequence.
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cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
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                                                                                                                                                                                                                                                                 1902 getetgggaggtgetgeeceageteageaaggaageeeteetgaagetgggeeegetgee 1961
                                                                                                           1842 cagcagcagttttgagggctacatagacttgggccgcgagctctccacacttcacgccct 1901
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569 TGTGGCCACCTACGACGCTATGTGGACCTGGCCCTGGAGCTTGCCACCCTGCACCTCCT 628
                                                                                                                                                                                                                                                                                                          Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
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/db_xref="taxon:7955"
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Location/Qualifiers
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Seq primer: T3 ET from Amersham
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Fax: 314 286 1810
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DEFINITION
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BE490923 628 bp mRNA EST 51-JUL-2000
AB486908.x1 Blackshear/Soares normalized Xenopus egg library Xenopus
laevis cDNA clone IMAGE:3300830 3' similar to TR:095174 095174
zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TATTAAAGCCCTGTACGAGTCGGATGAAAATTGTGAAGTATACCAATCAAAGTGCACGAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AGATCATCAGAGTGTTATGGTGTTATGGGTGTTGATTGTTGAGGNCTTTGCATCATGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GATGCATGANTAGICIGGGTCGAGGGAAGCAGGACATCAGICAGTGGGTTATCAGCGCAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CATTGAAGAATACCTCAATGTGGTGTTATAGAAGTACCTACATGATGCACTAGGTGAGTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 5.1%; Score 211.8; DB 27; Length 555; Best Local Similarity 65.9%; Pred. No. 1.1e 38;
                                                                                                                                                                                                                                                                                        2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 184; Indels
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us-09-294-298-3.rst

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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-MRI-BT0800-030
700-002-a02st3=2000-07-03st4=1)
Seq primer: pur 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magli,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE695645 516 bp mRNA EST 11-SEP-2000
MR1-BT0800-030700-002-a02 BT0800 Homo sapiens CDNA, mRNA sequence.
BE695645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
          567 gaaacccaacaaggacaacagccgccgggtagataacgtgctgaaactatggatcataga 626
                                                                                                                                                           239 TCAACCAAACAAGGATAACTGTCGCAGGGCAGAGAATGTACGGCTGTGGATCATTGA 180
                                                                                                                                                                                                                       627 agetegagagetgecececaagaagegatattaetgegagttatgeetggaegaeatget 686
                                                                                                                                                                                                                                                      179 GGCCAAGGACCTGCCAAAAAAAAAATTTCTGTGAACTTTGTCTGGACGATACTCT 120
                                                                                                                                                                                                                                                                                                                                             687 ctatgcacggaccaettccaagccccgctcagcctcaggagacactgtcttttggggcga 746
                                                                                                                                                                                                                                                                                                                                                                        sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 others
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/db_xref="taxon:9606"
/clone_lib="BT0800"
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High quality sequence stop: 268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 gcacttcgagtttaa 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ATATTTGAGTTTTA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                            Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: Stanpus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq primer: -400p from Gibco High quality sequence stop: 454.
, Martin,J., Hylie,T., Underwood,K., Theising,B., Bowers,Y., Person ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson, W. WashU Xenopus EST project, 1999 Other,ESTS: G)38908.yl Coher,ESTS: G)38908.yl Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 aggettectgageeggaggetaaaagetecateaaacgtacaaagteacaaeceaaaet 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 GGACCGGAACACACAGTTTCGAT-----TGCCTTCTTTCGTCCTGCTGAGAGCGACGA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Blackshear/Soares normalized Xenopus egg
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                WashU Xenopus EST project, 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="unfertilized egg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3300830"
                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.1%
Matches 350; Conservative
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ORIGIN
                                                                                                                            JOURNAL
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NCI_CGAP_Brn3, NCI_CGAP_LOS,

NCI_CGAP_Brn3, NCI_CGAP_LOS,

NCI_CGAP_LU19,

NCI_CGAP_LU19,

NCI_CGAP_LU14,

NCI_CGAP_LU14,

NCI_CGAP_LU14,

NCI_CGAP_LU14,

NCI_CGAP_LU14,

NCI_CGAP_LU15,

NCI_CGAP_LU16,

NCI_CGAP_LU16,

NCI_CGAP_LU16 mixture

was used as a tracer in a subtractive hybridization with

a driver whose composition is detailed below.

NCI_CGAP_Kid3 pool 1 LLAM 3334-337, 3682-3683,

NCI_CGAP_Kid3 pool 1 LLAM 3334-337, 3682-3683,

NCI_CGAP_LESS 1 NCI_CGAP_Kid5 pool 1 LLAM 338-3342,

1500522-150285; NCI_CGAP_Kid5 pool 1 LLAM 338-3342,

1471368-1477933, 1492104-149325); NCI_CGAP_LU5 pool 1

LLAM 3575-352, 3776-3778 (IMAGE CloneIDS 1474920-147791,

1520904-152349); NCI_CGAP_GC4 pool 1 LLAM 3164-3167,

3712-3725, 3776-3778 (IMAGE CloneIDS 1257096-1258631,

1469064-1470983, 1475592-1476743; NCI_CGAP_PC2 pool 1

LLAM 2457-2459, 2758-7759, 3062-3068 (IMAGE CloneIDS

985608-986759, 1101192-1101959, 1217928 1220615);

NCI_CGAP_COID pool 1 LLAM 264-2653, 2871-2872 (IMAGE

CloneIDS 1057416-1061255, 1144544-1145351), subtraction

was performed as previously described [Bonaldo, Lennon 6

Soares (1996): Normalization and Subtraction: Two

Approaches To Facilitate Gene Discovery. Genome Research

796_LIB=NCI_CGAP_GCA
NCI_CGAP_CLL1, NCI_CGAP_Lei2
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1217 acatggccatgtcagaggtagaccggttcatggagcgggaacacctcatattccgcgaga 1276
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IMAGE:3419073 5' similar to TR:09UJF2 09UJF2 DJ593C16.1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1277 acaegetegecaettaaagecatagaagagtatatgagaetgattggecagaaataeetea 1336
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Tel: (301) 496-1550
Banil: Robert Strausbergenih.gov
Digo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbry/mage/image.html
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/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT/T3b-Pac (Pharmacia) with a modified
polyliber; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library
derived from Bl. Bl constitutes a mixture of 21
normalized or subtracted NCI_CGAP_ libraries: NCI_CGAP_CO4
NCI_CGAP_PO22, NCI_CGAP_PT28, NCI_CGAP_CO10,
NCI_CGAP_CO16, NCI_CGAP_Rid5, NCI_CGAP_Eid12,
NCI_CGAP_Lid3, NCI_CGAP_Rid11, NCI_CGAP_Liym2,
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NATIONAL CANCER INStitute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW204612 347 bp mRNA EST 02-DEC-1999 UI-H-BII-aej-c-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens CDNA clone IMAGE:2719467 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1542 ctgtgcagagcggggccgggaggacattgctgacaggctgatcagcgcctcgctcttcct 1601
                                                                                                                                                                                1302 agagtatatgagactgattggccagaaatacctcaaggatgccattggggagttcatccg 1361
                                                                                                                                                                                                                                                                                                                                   1362 ggctctgtatgaatctgaggagaactgtgaagtagaccccatcaagtgcacagcgtccag 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1422 tctggcagagcaccaggccaacctgcggatgtgctgtgagttggccctgtgcaaggtggt 1481
                                                                                                                                                                                                                                                                                                                                                                             79 AGCGCTGTATGAGTCAGATGAGAACTGCGAAGTGGATCCCAGCAGCAAGTGGCTGA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 CCTCCCAGAGCACCAGGGCAACTCAGAATGTGCTGCGAGCTGGCCTTCTGCAAGATCAT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 CAACTCCTACTGTGTCTTCCCACGGGAGTTGAAAGAGGTGTTTGCCTCGTGGAGGCAGGA 258
                                                                                                         0; Gaps
                                                                                                                                                                                                                                                        19 AGGATACCTCAAGCTAGTGGGCCAGAAGTACCTGCAGGACGCCCTAGGTGAGTTCATCAA 78
                                 DB 111; Length 516;
                                                                                                         83; Indels
                         Match 4.8%; Score 197.2; DB 1 Local Similarity 74.8%; Pred. No. 2.6e-35; les 247; Conservative 0; Mismatches 83
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/db_xref="taxon:9606"
/clone="IMAGE:2719467"
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                                                                                                    Matches 247; Conservative
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3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pyTy3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento 181 c 151 g 129 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Tumor Gene Index
Uppublished (1997)
Other_ESTS: uw39f05.x1
Contact: Robert Strausberg, Ph.D.
Tel:: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1094885
Seq primer: -40RP from Gibco
High quality sequence stop: 461.
1 (bases 1 to 596)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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P-PSDB; W24227.
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This sequence encodes a protein capable of binding to active-type-R-Ras protein. The protein has a molecular weight of 98 kD by SDS-PAGE, and is designated 998. The protein coding sequence can be inserted into a suitable vector to treat certain tumours or diseases (various cancers) in which active R-Ras protein in involved. Because active R-Ras protein is involved in formation and inhibition of tumours and related to diseases in which cellular Ca ions or phospholipids are involved, the screening method can be used for screening e.g. a tumour forming promoter or tumour forming inhibitor.
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cancer, and diseases related to cellular calcium ion concentrations
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Pred. No. 1.9e-12;
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                          Claim 9; Page 9-12; 18pp; Japanese.
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(first entry)

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The present invention describes a library of human polynucleotides

comprising the sequences given in 21532 to 21779. Also described is a
method of detecting differentially expressed genes correlated with the
cancerous state of a mammalian cell, comprising detecting at least one
differentially expressed gene product in a test sample from a cell
suspected of being cancerous, where the gene product is encoded by one
of the 5248 polynucleotide sequences given in 212532 to 21779. The
of the 5248 polynucleotide sequences given in 212532 to 217779. The
polynucleotides can be used as a source of primers and probes, which can
be used for avariety of purpose, e.g. detection of expression levels,
mapping, tissue typing or profiling, forensics, genetic analysis and
detection of polymorphisms. Polypeptides encoded by the polynucleotides
can be used for raising antibodies for experimental, diagnostic and
therapeutic purposes. The polynucleotides may also be used to construct
arrays for diagnostics (which may be used to determine function of a
remoded protein); and to detect differences in expression levels between
two cells (e.g. to identify abnormal or diseased tissue in a human, to
identify a genetic predisposition or susceptibility to a disease such as
cancer). The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3748 tggccccaccttggaacggcctggccccccagccccaccccccaccccggctgcaga 3807
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                                                                   Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
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Human gene expression product cDNA sequence SEQ ID NO:4735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escobedo J, García PD, García V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dickson M, Drmanac R, Drmanac S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 63.6; DB 20; 33.0%; Pred. No. 2.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 2250-2251; 2479pp; English.
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98US-0072910.
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Escobedo J, Garri, ...
Jones WL, Kassam A, Ken ...
G, Leshkowitz D, sudduth
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                                                                                                                                                                                                                      Homo sapiens
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03-APR-1998;
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